

OM protein - protein search, using sw model

Run on: October 26, 2004, 19:13:50 ; Search time 194 Seconds
 (without alignments)
 14.829 Million cell updates/sec

Title: US-09-992-124B-34
 Perfect score: 31
 Sequence: 1 HKNQY 5

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%				
No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	87	2	Q92HN7	Q92hn7 rickettsia
2	31	100.0	104	2	Q6E6E2	Q6e6e2 nosema locu
3	31	100.0	169	2	Q49002	Q49002 mycoplasma
4	31	100.0	282	2	Q92DN1	Q92dn1 listeria in
5	31	100.0	299	2	Q7N6D1	Q7n6d1 photorhabdu
6	31	100.0	335	2	O07671	O07671 enterococcu
7	31	100.0	350	2	Q7P8P3	Q7p8p3 rickettsia
8	31	100.0	378	2	Q6LTS1	Q6lts1 photobacter
9	31	100.0	378	2	CAG19304	Cag19304 photobact
10	31	100.0	410	2	Q9VI96	Q9vi96 drosophila
11	31	100.0	437	2	Q7SYX5	Q7syx5 xenopus lae
12	31	100.0	651	2	Q9HFM9	Q9hfm9 glomus moss
13	31	100.0	746	2	Q84T47	Q84t47 oryza sativ
14	31	100.0	906	1	NUOG_BUCAI	P57257 buchnera ap
15	31	100.0	907	1	NUOG_BUCBP	Q89aul buchnera ap

16	31	100.0	910	1	NUOG_BUCAP	Q8k9y2	buchnera ap
17	31	100.0	934	2	Q6C5I3	Q6c5i3	yarrowia li
18	31	100.0	1575	2	Q9LCH3	Q9lch3	streptococc
19	31	100.0	1577	2	Q54178	Q54178	streptococc
20	31	100.0	1597	2	Q6BNN9	Q6bnn9	debaryomyce
21	31	100.0	1611	2	Q7RD43	Q7rd43	plasmodium
22	31	100.0	1998	2	Q8LJX1	Q8ljx1	sorghum bic
23	31	100.0	3026	2	Q8ILS9	Q8ils9	plasmodium
24	28	90.3	78	2	Q86M23	Q86m23	apis dorsat
25	28	90.3	82	2	Q9PCU4	Q9pcu4	xylella fas
26	28	90.3	152	2	Q8NLK8	Q8nlk8	corynebacte
27	28	90.3	152	2	CAF20958	Caf20958	corynebac
28	28	90.3	200	2	Q6LTA9	Q6lta9	photobacter
29	28	90.3	200	2	CAG19467	Cag19467	photobact
30	28	90.3	225	2	Q81991	Q81991	human papil
31	28	90.3	260	2	Q6XSP3	Q6xsp3	oncorhynchu
32	28	90.3	260	2	AAP12640	Aap12640	oncorhync
33	28	90.3	265	2	Q9CHK7	Q9chk7	lactococcus
34	28	90.3	286	1	PARB_RICPR	Q9ze87	rickettsia
35	28	90.3	289	2	Q9BX01	Q9bx01	homo sapien
36	28	90.3	308	2	Q6CWF9	Q6cwf9	kluyveromyc
37	28	90.3	312	2	Q73HR3	Q73hr3	wolbachia p
38	28	90.3	312	2	AAS14200	Aas14200	wolbachia
39	28	90.3	341	2	Q6XGF2	Q6xgf2	escherichia
40	28	90.3	341	2	Q74YT2	Q74yt2	yersinia pe
41	28	90.3	341	2	AAP70289	Aap70289	escherich
42	28	90.3	341	2	AAS58621	Aas58621	yersinia
43	28	90.3	351	2	Q935B9	Q935b9	salmonella
44	28	90.3	363	2	Q7QEZ5	Q7qez5	anopheles g
45	28	90.3	373	2	Q8ABQ6	Q8abq6	bacteroides

ALIGNMENTS

RESULT 1

Q92HN7

ID Q92HN7 PRELIMINARY; PRT; 87 AA.
AC Q92HN7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RC0734;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).

DR EMBL; AE008631; AAL03272.1; -.
DR PIR; F97791; F97791.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 87 AA; 9809 MW; B0D078C34C1D6F0A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 20 HKNQY 24

Search completed: October 26, 2004, 19:39:07
Job time : 198 secs

OM protein - protein search, using sw model

Run on: October 26, 2004, 19:15:00 ; Search time 37 Seconds
(without alignments)
13.002 Million cell updates/sec

Title: US-09-992-124B-34
Perfect score: 31
Sequence: 1 HKNQY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	31	100.0	87	2	F97791	hypothetical prote
2	31	100.0	169	2	S77804	hypothetical prote
3	31	100.0	282	2	AF1530	conserved hypothet
4	31	100.0	906	2	E84948	NADH2 dehydrogenas
5	28	90.3	82	2	H82652	hypothetical prote
6	28	90.3	225	2	S48780	L1 protein - human
7	28	90.3	265	2	D86715	conserved hypothet
8	28	90.3	286	2	C71714	stage 0 sporulatio
9	28	90.3	351	2	T17246	hypothetical prote
10	28	90.3	673	2	T15551	hypothetical prote
11	28	90.3	735	2	D70174	methyl-accepting c
12	28	90.3	1447	2	F82909	hypothetical prote
13	28	90.3	2351	2	G71415	hypothetical prote

14	27	87.1	127	2	T27727	hypothetical prote
15	27	87.1	232	2	G69703	sapB protein [impo
16	27	87.1	240	2	AG0605	oxygen-insensitive
17	27	87.1	256	1	QQCVPP	BR1 protein - pota
18	27	87.1	256	2	A40169	protein-tyrosine-p
19	27	87.1	256	2	JQ2304	BL1 protein - pepp
20	27	87.1	256	2	S31872	BR1 protein - pepp
21	27	87.1	257	1	JQ1873	BR1 protein - toma
22	27	87.1	257	1	QQCVW5	BV1 protein - abut
23	27	87.1	274	2	A25102	reaction center pr
24	27	87.1	288	2	T34151	hypothetical prote
25	27	87.1	328	2	A35257	replication protei
26	27	87.1	379	2	E81334	Ni/Fe-hydrogenase
27	27	87.1	434	2	C82885	membrane nuclease
28	27	87.1	446	2	S22614	hypothetical prote
29	27	87.1	450	2	S73139	hypothetical prote
30	27	87.1	585	2	F83913	hypothetical prote
31	27	87.1	644	2	F81411	probable ribonucle
32	27	87.1	668	2	E89783	hypothetical prote
33	27	87.1	770	2	AI2421	hypothetical prote
34	27	87.1	822	1	TVHUFE	protein-tyrosine k
35	27	87.1	1054	2	G82934	hypothetical prote
36	27	87.1	1154	2	T39663	paired amphipathic
37	27	87.1	1422	2	T42636	protein-tyrosine-p
38	27	87.1	1442	1	B48148	protein-tyrosine-p
39	27	87.1	1445	1	A48148	protein-tyrosine-p
40	27	87.1	1506	2	T30886	integumentary muc
41	27	87.1	1585	2	T19121	probable protein-t
42	27	87.1	1751	2	T09394	gag-pro-pol polypr
43	27	87.1	2150	1	GNNYH2	genome polyprotein
44	27	87.1	2157	1	GNNY1B	genome polyprotein
45	27	87.1	2314	1	A46151	protein-tyrosine-p

ALIGNMENTS

RESULT 1

F97791

hypothetical protein RC0734 [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97791

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Roux, V.; Cossart, P.; Weissenbach, J.; Claverie, J.M.; Raoult, D. Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: F97791

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-87 <KUR>

A;Cross-references: UNIPROT:Q92HN7; GB:AE006914; PIDN:AAL03272.1; PID:g15619828; GSPDB:GN00173

C;Genetics:

A;Gene: RC0734

Query Match 100.0%; Score 31; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 20 HKNQY 24

Search completed: October 26, 2004, 19:39:49
Job time : 39 secs

OM protein - protein search, using sw model

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Run on:      October 26, 2004, 19:39:16 ; Search time 127 Seconds
              (without alignments)
              12.746 Million cell updates/sec
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Title: US-09-992-124B-34
Perfect score: 31
Sequence: 1 HKNQY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	5	10	US-09-992-124A-34	Sequence 34, Appl
2	31	100.0	194	16	US-10-767-701-57863	Sequence 57863, A
3	31	100.0	218	15	US-10-425-114-51940	Sequence 51940, A
4	31	100.0	227	15	US-10-425-114-54655	Sequence 54655, A
5	31	100.0	327	10	US-09-782-974C-66	Sequence 66, Appl
6	31	100.0	360	14	US-10-357-886-34	Sequence 34, Appl
7	31	100.0	605	16	US-10-437-963-141422	Sequence 141422,
8	31	100.0	997	16	US-10-437-963-187883	Sequence 187883,
9	31	100.0	1998	15	US-10-389-566-1643	Sequence 1643, Ap
10	28	90.3	50	9	US-09-796-692-2436	Sequence 2436, Ap
11	28	90.3	50	14	US-10-040-862-2436	Sequence 2436, Ap
12	28	90.3	50	15	US-10-057-475B-2436	Sequence 2436, Ap
13	28	90.3	50	15	US-10-154-884B-2436	Sequence 2436, Ap
14	28	90.3	50	16	US-10-764-324-2436	Sequence 2436, Ap
15	28	90.3	86	16	US-10-767-701-61462	Sequence 61462, A
16	28	90.3	152	9	US-09-738-626-6735	Sequence 6735, Ap
17	28	90.3	206	15	US-10-424-599-219720	Sequence 219720,
18	28	90.3	426	9	US-09-731-872-310	Sequence 310, App
19	28	90.3	426	9	US-09-731-872-317	Sequence 317, App
20	28	90.3	426	10	US-09-876-997-310	Sequence 310, App
21	28	90.3	426	10	US-09-876-997-317	Sequence 317, App
22	28	90.3	426	16	US-10-655-601-5	Sequence 5, Appli
23	28	90.3	481	9	US-09-731-872-415	Sequence 415, App
24	28	90.3	481	10	US-09-876-997-415	Sequence 415, App
25	28	90.3	615	15	US-10-320-797-3255	Sequence 3255, Ap
26	28	90.3	621	14	US-10-447-013-2	Sequence 2, Appli
27	28	90.3	621	14	US-10-447-013-26	Sequence 26, Appl
28	28	90.3	1332	9	US-09-982-091A-4	Sequence 4, Appli
29	27	87.1	9	14	US-10-286-457-230	Sequence 230, App
30	27	87.1	34	9	US-09-764-869-1227	Sequence 1227, Ap
31	27	87.1	34	14	US-10-091-504-1227	Sequence 1227, Ap
32	27	87.1	34	15	US-10-227-577-1227	Sequence 1227, Ap
33	27	87.1	55	15	US-10-424-599-167189	Sequence 167189,
34	27	87.1	71	15	US-10-424-599-202605	Sequence 202605,
35	27	87.1	86	15	US-10-424-599-179037	Sequence 179037,
36	27	87.1	107	15	US-10-424-599-281748	Sequence 281748,
37	27	87.1	117	16	US-10-437-963-138519	Sequence 138519,
38	27	87.1	120	15	US-10-276-774-1859	Sequence 1859, Ap
39	27	87.1	137	15	US-10-424-599-277923	Sequence 277923,
40	27	87.1	147	15	US-10-424-599-280933	Sequence 280933,
41	27	87.1	148	11	US-09-864-408A-3204	Sequence 3204, Ap
42	27	87.1	150	16	US-10-437-963-176854	Sequence 176854,
43	27	87.1	175	9	US-09-968-415-8	Sequence 8, Appli
44	27	87.1	175	14	US-10-180-719-8	Sequence 8, Appli
45	27	87.1	230	9	US-09-922-217-1060	Sequence 1060, Ap

ALIGNMENTS

RESULT 1
 US-09-992-124A-34
 ; Sequence 34, Application US/09992124A
 ; Publication No. US20030162289A1


```
; GENERAL INFORMATION:
; APPLICANT: Heidaran, Mohammad A.
; APPLICANT: Haaland, Perry D.
; APPLICANT: Wilkins, Jamie H.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion
; FILE REFERENCE: 102-410
; CURRENT APPLICATION NUMBER: US/09/992,124A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide selected for biological activity
US-09-992-124A-34
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Query Match          100.0%; Score 31; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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```
Qy      1 HKNQY 5
        |||||
Db      1 HKNQY 5
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RESULT 2

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US-10-767-701-57863
; Sequence 57863, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 57863
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30973132.pep
US-10-767-701-57863
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Query Match          100.0%; Score 31; DB 16; Length 194;
Best Local Similarity 100.0%; Pred. No. 82;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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Qy      1 HKNQY 5
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Db |||||
29 HKNQY 33

RESULT 3

US-10-425-114-51940
; Sequence 51940, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51940
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700616516_FLI.pep
US-10-425-114-51940

Query Match 100.0%; Score 31; DB 15; Length 218;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
 |||||
Db 135 HKNQY 139

RESULT 4

US-10-425-114-54655
; Sequence 54655, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 54655
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-192-F7_FLI.pep
US-10-425-114-54655

Query Match 100.0%; Score 31; DB 15; Length 227;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
| | | | |
Db 198 HKNQY 202

RESULT 5

US-09-782-974C-66

; Sequence 66, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-782-974C-66

Query Match 100.0%; Score 31; DB 10; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 256 HKNQY 260

RESULT 6

US-10-357-886-34

; Sequence 34, Application US/10357886
; Publication No. US20030159170A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fader, Gary M.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
; FILE REFERENCE: BB1328 US NA
; CURRENT APPLICATION NUMBER: US/10/357,886
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US/09/501,115
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/119,585
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Glycine max
US-10-357-886-34

Query Match 100.0%; Score 31; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 22 HKNQY 26

RESULT 7

US-10-437-963-141422

; Sequence 141422, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

```

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141422
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(605)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42527C.1.pep
US-10-437-963-141422

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Query Match          100.0%; Score 31; DB 16; Length 605;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HKNQY 5
        |||||
Db      179 HKNQY 183

```

RESULT 8

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US-10-437-963-187883
; Sequence 187883, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187883
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_84542C.1.pep
US-10-437-963-187883

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```

Query Match          100.0%; Score 31; DB 16; Length 997;

```

Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 186 HKNQY 190

RESULT 9

US-10-389-566-1643
; Sequence 1643, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1643
; LENGTH: 1998
; TYPE: PRT
; ORGANISM: Sorghum bicolor
US-10-389-566-1643

Query Match 100.0%; Score 31; DB 15; Length 1998;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 1348 HKNQY 1352

RESULT 10

US-09-796-692-2436
; Sequence 2436, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2436
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2436

Query Match 90.3%; Score 28; DB 9; Length 50;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|:|
Db 26 HRNQY 30

RESULT 11
US-10-040-862-2436
; Sequence 2436, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126

```

; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2436
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-040-862-2436

```

```

Query Match          90.3%;   Score 28;   DB 14;   Length 50;
Best Local Similarity 80.0%;   Pred. No. 96;
Matches      4;   Conservative      1;   Mismatches      0;   Indels      0;   Gaps      0;

```

```

Qy          1 HKNQY 5
             |:|
Db          26 HRNQY 30

```

RESULT 12

```

US-10-057-475B-2436
; Sequence 2436, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation

```



```

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2436
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2436

```

```

Query Match          90.3%; Score 28; DB 15; Length 50;
Best Local Similarity 80.0%; Pred. No. 96;
Matches      4; Conservative 1; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HKNQY 5
        |:|||
Db      26 HRNQY 30

```

```

RESULT 13
US-10-154-884B-2436
; Sequence 2436, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
Therapy of
; TITLE OF INVENTION: Hematological Malignancies

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```

; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2436
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-2436

```

```

Query Match          90.3%; Score 28; DB 15; Length 50;
Best Local Similarity 80.0%; Pred. No. 96;
Matches      4; Conservative 1; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HKNQY 5
        |:|||
Db      26 HRNQY 30

```

```

RESULT 14
US-10-764-324-2436
; Sequence 2436, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23

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; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2436
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-764-324-2436

```

```

Query Match          90.3%;   Score 28;   DB 16;   Length 50;
Best Local Similarity 80.0%;   Pred. No. 96;
Matches      4;   Conservative    1;   Mismatches    0;   Indels    0;   Gaps    0;

```

```

Qy          1 HKNQY 5
             |:|||
Db          26 HRNQY 30

```

RESULT 15

```

US-10-767-701-61462
; Sequence 61462, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 61462
;   LENGTH: 86
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor

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; FEATURE:
; OTHER INFORMATION: Clone ID: 9307826.pep
US-10-767-701-61462

Query Match 90.3%; Score 28; DB 16; Length 86;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|:|
Db 50 HRNQY 54

Search completed: October 26, 2004, 19:50:51
Job time : 128 secs

OM protein - protein search, using sw model

Run on: October 26, 2004, 19:33:11 ; Search time 39 Seconds
 (without alignments)
 8.502 Million cell updates/sec

Title: US-09-992-124B-34
 Perfect score: 31
 Sequence: 1 HKNQY 5

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	31	100.0	188	4	US-09-248-796A-21795	Sequence 21795, A
2	31	100.0	360	4	US-09-501-115-34	Sequence 34, Appl
3	28	90.3	58	4	US-09-513-999C-7526	Sequence 7526, Ap
4	28	90.3	73	4	US-09-248-796A-22573	Sequence 22573, A
5	28	90.3	342	4	US-09-543-681A-5131	Sequence 5131, Ap
6	28	90.3	342	4	US-09-489-039A-14092	Sequence 14092, A
7	28	90.3	621	4	US-09-331-568A-2	Sequence 2, Appli
8	28	90.3	621	4	US-09-331-568A-26	Sequence 26, Appl
9	27	87.1	96	4	US-09-248-796A-18319	Sequence 18319, A
10	27	87.1	97	4	US-09-248-796A-23466	Sequence 23466, A
11	27	87.1	97	4	US-09-248-796A-25700	Sequence 25700, A

12	27	87.1	100	4	US-09-513-999C-7353	Sequence 7353, Ap
13	27	87.1	175	3	US-09-008-271A-8	Sequence 8, Appli
14	27	87.1	223	4	US-09-543-681A-5818	Sequence 5818, Ap
15	27	87.1	242	1	US-08-015-985-7	Sequence 7, Appli
16	27	87.1	242	4	US-09-280-597-7	Sequence 7, Appli
17	27	87.1	245	1	US-08-015-985-8	Sequence 8, Appli
18	27	87.1	245	4	US-09-280-597-8	Sequence 8, Appli
19	27	87.1	248	1	US-08-015-985-9	Sequence 9, Appli
20	27	87.1	248	4	US-09-280-597-9	Sequence 9, Appli
21	27	87.1	260	2	US-08-685-992-4	Sequence 4, Appli
22	27	87.1	260	2	US-08-685-992-25	Sequence 25, Appl
23	27	87.1	260	2	US-09-144-925-4	Sequence 4, Appli
24	27	87.1	260	2	US-09-144-925-25	Sequence 25, Appl
25	27	87.1	261	2	US-08-685-992-3	Sequence 3, Appli
26	27	87.1	261	2	US-09-144-925-3	Sequence 3, Appli
27	27	87.1	263	2	US-08-685-992-5	Sequence 5, Appli
28	27	87.1	263	2	US-09-144-925-5	Sequence 5, Appli
29	27	87.1	272	4	US-09-543-681A-4916	Sequence 4916, Ap
30	27	87.1	276	4	US-09-540-236-3192	Sequence 3192, Ap
31	27	87.1	312	3	US-09-134-001C-3465	Sequence 3465, Ap
32	27	87.1	466	4	US-09-248-796A-19009	Sequence 19009, A
33	27	87.1	471	2	US-08-477-451-20	Sequence 20, Appl
34	27	87.1	822	4	US-09-886-319A-64	Sequence 64, Appl
35	27	87.1	822	4	US-09-538-092-941	Sequence 941, App
36	27	87.1	1442	1	US-08-015-986A-3	Sequence 3, Appli
37	27	87.1	1442	2	US-08-446-363-3	Sequence 3, Appli
38	27	87.1	1445	1	US-08-015-986A-2	Sequence 2, Appli
39	27	87.1	1445	2	US-08-446-363-2	Sequence 2, Appli
40	27	87.1	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
41	27	87.1	2308	1	US-08-015-973-1	Sequence 1, Appli
42	27	87.1	2308	2	US-08-448-164-1	Sequence 1, Appli
43	27	87.1	2308	3	US-08-081-929-2	Sequence 2, Appli
44	27	87.1	2314	4	US-09-816-703A-2	Sequence 2, Appli
45	26	83.9	91	4	US-09-248-796A-26461	Sequence 26461, A

ALIGNMENTS

RESULT 1

US-09-248-796A-21795

; Sequence 21795, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 21795

; LENGTH: 188
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21795

Query Match 100.0%; Score 31; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 108 HKNQY 112

RESULT 2

US-09-501-115-34
; Sequence 34, Application US/09501115
; Patent No. 6552249
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fader, Gary M.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
; FILE REFERENCE: BB1328 US NA
; CURRENT APPLICATION NUMBER: US/09/501,115
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,585
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Glycine max
US-09-501-115-34

Query Match 100.0%; Score 31; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 22 HKNQY 26

Search completed: October 26, 2004, 19:48:23
Job time : 40 secs

OM protein - protein search, using sw model

Run on: October 26, 2004, 19:08:30 ; Search time 159 Seconds
(without alignments)
11.281 Million cell updates/sec

Title: US-09-992-124B-34
Perfect score: 31
Sequence: 1 HKNQY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	31	100.0	5	6	AAO30049	Aao30049 Peptide #
2	31	100.0	146	4	AAU55892	Aau55892 Propionib
3	31	100.0	146	6	ABM52411	Abm52411 Propionib
4	31	100.0	313	6	ABM68943	Abm68943 Photorhab
5	31	100.0	327	4	AAG80961	Aag80961 Human nGP
6	31	100.0	327	5	ABG93779	Abg93779 Human G p
7	31	100.0	360	6	ADA38409	Ada38409 Soybean c
8	31	100.0	360	7	ADG88759	Adg88759 Soy bean
9	31	100.0	410	4	ABB64830	Abb64830 Drosophil

10	31	100.0	532	7	ADB67810	Adb67810	Human lun
11	31	100.0	1998	8	ADJ49639	Adj49639	Oil-assoc
12	28	90.3	50	4	AAM82072	Aam82072	Human hae
13	28	90.3	53	4	AAU60734	Aau60734	Propionib
14	28	90.3	53	6	ABM57253	Abm57253	Propionib
15	28	90.3	58	3	AAG03445	Aag03445	Human sec
16	28	90.3	152	4	AAG92981	Aag92981	C glutami
17	28	90.3	225	2	AAR88270	Aar88270	Papilloma
18	28	90.3	265	5	ABB54037	Abb54037	Lactococc
19	28	90.3	342	7	ADF04846	Adf04846	Bacterial
20	28	90.3	342	7	ABO67575	Abo67575	Klebsiell
21	28	90.3	353	4	AAM41451	Aam41451	Human pol
22	28	90.3	426	3	AAB42986	Aab42986	Human ORF
23	28	90.3	426	4	AAM39665	Aam39665	Human pol
24	28	90.3	426	4	AAB94867	Aab94867	Human pro
25	28	90.3	426	4	AAG89197	Aag89197	Human sec
26	28	90.3	426	4	AAG89190	Aag89190	Human sec
27	28	90.3	426	7	ADC06747	Adc06747	Human ino
28	28	90.3	426	8	ADM72106	Adm72106	Human tau
29	28	90.3	474	3	AAB07947	Aab07947	A uridine
30	28	90.3	481	4	AAG89295	Aag89295	Human sec
31	28	90.3	615	7	ADB70211	Adb70211	C. neofor
32	28	90.3	621	2	AAW62842	Aaw62842	Helicobac
33	28	90.3	1332	5	AAU97587	Aau97587	Human Cla
34	28	90.3	1332	7	ADC31665	Adc31665	Human nov
35	27	87.1	9	7	ADC44502	Adc44502	Endotheli
36	27	87.1	15	4	AAG65155	Aag65155	Human cyt
37	27	87.1	21	7	ADC27554	Adc27554	Human col
38	27	87.1	24	3	AAB01490	Aab01490	Lectin po
39	27	87.1	30	4	AAO02806	Aao02806	Human pol
40	27	87.1	34	4	AAU22453	Aau22453	Human car
41	27	87.1	34	7	ADE46421	Ade46421	Human car
42	27	87.1	44	5	ADK34613	Adk34613	Novel hum
43	27	87.1	44	5	ADK34347	Adk34347	Novel hum
44	27	87.1	81	5	ABP02651	Abp02651	Human ORF
45	27	87.1	95	4	ABG21748	Abg21748	Novel hum

ALIGNMENTS

RESULT 1

AAO30049

ID AAO30049 standard; peptide; 5 AA.

XX

AC AAO30049;

XX

DT 03-SEP-2003 (first entry)

XX

DE Peptide #19 used to enhance cell secretion, alternative version.

XX

KW Cellular adhesion; growth; expression; secretion.

XX

OS Unidentified.

XX

PN WO2003044045-A2.

XX

PD 30-MAY-2003.
 XX
 PF 19-NOV-2002; 2002WO-US037207.
 XX
 PR 19-NOV-2001; 2001US-00992124.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 XX
 PI Campbell RL, Heidaran M, Spargo CA, Wilkins JH, Haaland PD;
 XX
 DR WPI; 2003-482396/45.
 XX
 PT New peptide, useful for enhancing cell growth and/or secretion in a cell
 PT culture system.
 XX
 PS Claim 4; Page 66; 78pp; English.
 XX
 CC The invention relates to peptides having cell adhesion, growth,
 CC expression or secretion-enhancing activities. The peptides of the
 CC invention are useful for enhancing cell growth and/or secretion in a cell
 CC culture system. The present sequence is a peptide used to enhance cell
 CC secretion. Note: This sequence SEQ ID NO:34 is stated to be similar to
 CC the sequence shown in page 45 (AA030011). However these sequences differ
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 31; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
 |||||
 Db 1 HKNQY 5

RESULT 2
 AAU55892

ID AAU55892 standard; protein; 146 AA.
 XX
 AC AAU55892;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #16788.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.

XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59572.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 17087; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 31; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
 |||||
 Db 92 HKNQY 96

RESULT 3
 ABM52411
 ID ABM52411 standard; protein; 146 AA.
 XX
 AC ABM52411;
 XX

DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #17087.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglass J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64501.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 17087; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 31; DB 6; Length 146;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 92 HKNQY 96

RESULT 4

ABM68943

ID ABM68943 standard; protein; 313 AA.

XX

AC ABM68943;

XX

DT 20-NOV-2003 (first entry)

XX

DE Photorhabdus luminescens protein sequence #2040.

XX

KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.

XX

OS Photorhabdus luminescens.

XX

PN WO200294867-A2.

XX

PD 28-NOV-2002.

XX

PF 07-FEB-2002; 2002WO-IB003040.

XX

PR 07-FEB-2001; 2001FR-00001659.

XX

PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;

XX

DR WPI; 2003-148459/14.

XX

PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX

PS Claim 2; SEQ ID NO 2040; 1205pp; French.

XX

CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification
CC of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than *P. luminescens* and are able to alter
CC response or sensitivity to toxins and antibiotics produced by *P.*
CC *luminescens*. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which *P.*
CC *luminescens* is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated *P. luminescens* proteins

XX

SQ Sequence 313 AA;

Query Match 100.0%; Score 31; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKNQY 5
|||||
Db 297 HKNQY 301

RESULT 5

AAG80961

ID AAG80961 standard; protein; 327 AA.

XX

AC AAG80961;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR57.

XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder/attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW neuroprotective.

XX

OS Homo sapiens.

XX

PN WO200136473-A2.

XX

PD 25-MAY-2001.

XX

PF 16-NOV-2000; 2000WO-US031581.

XX

PR 16-NOV-1999; 99US-0165838P.

PR 17-NOV-1999; 99US-0166071P.
PR 19-NOV-1999; 99US-0166678P.
PR 28-DEC-1999; 99US-0173396P.
PR 22-FEB-2000; 2000US-0184129P.
PR 28-FEB-2000; 2000US-0185421P.
PR 28-FEB-2000; 2000US-0185554P.
PR 02-MAR-2000; 2000US-0186530P.
PR 03-MAR-2000; 2000US-0186811P.
PR 09-MAR-2000; 2000US-0188114P.
PR 17-MAR-2000; 2000US-0190310P.
PR 21-MAR-2000; 2000US-0190800P.
PR 20-APR-2000; 2000US-0198568P.
PR 02-MAY-2000; 2000US-0201190P.
PR 08-MAY-2000; 2000US-0203111P.
PR 25-MAY-2000; 2000US-0207094P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;

XX

DR WPI; 2001-389826/41.

DR N-PSDB; AAH51001.

XX

PT New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
PT useful for diagnosing and treating e.g. schizophrenia.

XX

PS Claim 37; Page 86; 261pp; English.

XX

CC The present invention relates to novel G protein-coupled receptors
CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC one such G protein-coupled receptor. GPCRs are also known as seven
CC transmembrane receptors and function in signal transduction. The nGPCRx
CC coding sequences are useful for screening a human to diagnose a disorder
CC affecting the brain or a genetic predisposition, specifically
CC schizophrenia. nGPCRx are useful for identifying compounds useful for
CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC metabolic and cardiovascular diseases, proliferative disorders and
CC hormonal disorders. Modulators of nGPCRx activity have the utility for
CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease

XX

SQ Sequence 327 AA;

Query Match 100.0%; Score 31; DB 4; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 HKNQY 5

Db |||||
 256 HKNQY 260

RESULT 6

ABG93779

ID ABG93779 standard; protein; 327 AA.

XX

AC ABG93779;

XX

DT 26-NOV-2002 (first entry)

XX

DE Human G protein-coupled receptor protein, beGPCR-seq57.

XX

KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;

KW nG protein coupled receptor; communication; serpentine structure;

KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;

KW genetic predisposition; brain; immune response; gene therapy;

KW anxiety disorder; depression; bipolar disorder; schizophrenia;

KW Huntington's disease; dyskinesia; manic depression; stroke;

KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;

KW tranquiliser.

XX

OS Homo sapiens.

XX

PN WO200264789-A1.

XX

PD 22-AUG-2002.

XX

PF 14-FEB-2001; 2001WO-US004641.

XX

PR 14-FEB-2001; 2001WO-US004641.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Lind P, Parodi LA, Vogeli G, Wood LS;

XX

DR WPI; 2002-674879/72.

DR N-PSDB; ABS70234.

XX

PT New nucleic acids and polypeptides of the nG protein-coupled receptor,

PT useful for treating or diagnosing a mental disorder or a disorder

PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or

PT Parkinson's disease.

XX

PS Example 1; Page 81; 244pp; English.

XX

CC The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nGPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or

CC polynucleotide and/or modulates its biological activity, for screening a
 CC human subject to diagnose a disorder, or a genetic predisposition to a
 CC disorder, affecting the brain or a genetic disposition to the disorder,
 CC for identifying compounds useful for the treatment of a mental disorder
 CC and for identifying a compound useful as a modulator of binding between
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
 CC useful for inducing an immune response in a mammal. The nucleic acid or
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
 CC be used for treating diabetes, inflammation or wounds. The sequences
 CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
 CC referred to as beGPCRs) proteins

XX

SQ Sequence 327 AA;

Query Match 100.0%; Score 31; DB 5; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
 |||||
 Db 256 HKNQY 260

RESULT 7

ADA38409

ID ADA38409 standard; protein; 360 AA.

XX

AC ADA38409;

XX

DT 20-NOV-2003 (first entry)

XX

DE Soybean cinnamyl-alcohol dehydrogenase type 5 #2.

XX

KW soybean; cinnamyl-alcohol dehydrogenase type 5; CAD; transgenic; plant;
 KW enzyme.

XX

OS Glycine max.

XX

PN US6552249-B1.

XX

PD 22-APR-2003.

XX

PF 09-FEB-2000; 2000US-00501115.

XX

PR 10-FEB-1999; 99US-0119585P.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX

PI Cahoon RE, Fader GM, Rafalski JA;

XX

DR WPI; 2003-615312/58.

DR N-PSDB; ADA38408.

XX

PT Novel nucleic acid molecule encoding corn cinnamyl-alcohol dehydrogenase

PT useful for producing transgenic plants having altered levels of lignin
PT biosynthetic enzyme.

XX

PS Example 2; Col 73-74; 47pp; English.

XX

CC The invention relates to an isolated polynucleotide comprising a
CC nucleotide sequence encoding a polypeptide having corn cinnamyl-alcohol
CC dehydrogenase (CAD) activity. The polynucleotide is useful for
CC transforming a cell and producing a transgenic plant. The polynucleotide
CC is also useful for selecting an isolated polynucleotide that affects the
CC level of expression of a CAD or a CAD-related polypeptide in a host cell,
CC preferably a plant cell. Nucleic acid fragments of the polynucleotide are
CC useful to create transgenic plants in which CAD polypeptides are present
CC at higher or lower levels than normal or in cell types or developmental
CC stages in which they are not normally found. The nucleic acid fragments
CC are also useful as probes for genetically and physically mapping the
CC genes that they are a portion and as markers for traits linked to those
CC genes. Such information is useful in plant breeding to develop lines with
CC desired phenotypes. The nucleic acid fragments are also useful as
CC restriction fragment length polymorphism (RFLP) markers, for physical
CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.
CC The present sequence represents the amino acid sequence of the soybean
CC cinnamyl-alcohol dehydrogenase type 5 #2.

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 31; DB 6; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKNQY 5

|||||

Db 22 HKNQY 26

RESULT 8

ADG88759

ID ADG88759 standard; protein; 360 AA.

XX

AC ADG88759;

XX

DT 11-MAR-2004 (first entry)

XX

DE Soy bean cinnamyl-alcohol dehydrogenase type 5 EST protein #2.

XX

KW Cinnamyl-alcohol dehydrogenase; cell wall architecture; host defence;
KW injury; repair mechanism; plant; soy bean; expressed sequence tag; EST;
KW enzyme.

XX

OS Glycine max.

XX

PN US2003159170-A1.

XX

PD 21-AUG-2003.

XX

PF 04-FEB-2003; 2003US-00357886.

XX

PR 10-FEB-1999; 99US-0119585P.
 PR 09-FEB-2000; 2000US-00501115.
 XX
 PA (CAHO/) CAHOON R C.
 XX
 PI Cahoon RC;
 XX
 DR WPI; 2003-787369/74.
 DR N-PSDB; ADG88758.
 XX
 PT New polynucleotide encoding a polypeptide having cinnamyl-alcohol
 PT dehydrogenase activity, useful for providing mechanisms to control cell
 PT wall architecture, host defense or injury repair mechanisms in plant
 PT cells.
 XX
 PS Example 3; SEQ ID NO 34; 49pp; English.
 XX
 CC The present invention relates to a new isolated polynucleotide comprising
 CC a nucleotide sequence encoding a polypeptide having cinnamyl-alcohol
 CC dehydrogenase activity. The invention is useful for providing genetic
 CC tools to enhance or alter lignin biosynthesis, which in turn could
 CC provide mechanisms to control cell wall architecture, host defence or
 CC injury repair mechanisms and reduce the pool of phenolic compounds in
 CC plant cells. The present sequence is soy bean cinnamyl-alcohol
 CC dehydrogenase expressed sequence tag (EST) protein.
 XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 31; DB 7; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
 |||||
 Db 22 HKNQY 26

RESULT 9

ABB64830

ID ABB64830 standard; protein; 410 AA.

XX

AC ABB64830;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 21282.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US009231.

XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL08933.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 21282; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 410 AA;

Query Match 100.0%; Score 31; DB 4; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKNQY 5
 |||||
 Db 219 HKNQY 223

RESULT 10

ADB67810

ID ADB67810 standard; protein; 532 AA.

XX

AC ADB67810;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human lung specific protein sequence SEQ ID NO:93.

XX

KW human; lung specific polypeptide; LSP; lung specific nucleic acid; LSNA;

KW lung; cytostatic; vaccine; gene therapy; immune response; lung cancer;

KW metastasis.

XX

OS Homo sapiens.

XX

PN WO2003020899-A2.

XX

PD 13-MAR-2003.
XX
PF 29-AUG-2002; 2002WO-US027771.
XX
PR 31-AUG-2001; 2001US-0316260P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Liu C, Chen S;
XX
DR WPI; 2003-300880/29.
DR N-PSDB; ADB67902.
XX
PT Novel lung specific polypeptides and nucleic acids, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous disease states in lung.
XX
PS Example 1; Page 222-224; 263pp; English.
XX
CC The present invention describes human lung specific polypeptides (LSP,
CC (I)) and lung specific nucleic acids (LSNA, (II)). Also described: (1)
CC determining (M1) the presence of an LSNA in a sample; (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a polypeptide (IV)
CC encoded by (II); (5) production of (IV); (6) an antibody (V) or its
CC fragment that specifically binds to an LSP; (7) determining (M2) the
CC presence of an LSP in a sample; (8) a kit for detecting a risk of cancer
CC or presence of cancer in a patient, comprising a unit for determining the
CC presence of (I) or (II) in a sample of the patient; and (9) a vaccine
CC comprising (I) or (II). LSP and LSNA sequences have cytostatic
CC activities, and can be used in vaccines, gene therapy, and as inducers of
CC an immune response. (I) and (II) can be used for diagnosing or monitoring
CC the presence and metastases of lung cancer in a patient, by determining
CC the amount of (I) or (II) in a sample of a patient, and comparing the
CC amount of the determined nucleic acid molecule or the polypeptide in the
CC sample of the patient to the amount of the lung specific marker in a
CC normal control, where the difference in the amount of the nucleic acid
CC molecule or the polypeptide in the sample compared to the amount of the
CC nucleic acid molecule or the polypeptide in the normal control is
CC associated with the presence of lung cancer. (I) and (V) are useful for
CC treating a patient with lung cancer, by administering (I) or (V), where
CC the administration of (I) or (V) induces an immune response against the
CC lung cancer cell expressing the nucleic acid molecule or a polypeptide.
CC (I), (II) and (V) are also useful for identifying, diagnosing,
CC monitoring, staging, imaging and treating lung cancer and non-cancerous
CC disease states in lung, for identifying lung tissue, and monitoring,
CC identifying and/or designing agonists and antagonists of (I). (II) can be
CC used in gene therapy, for producing transgenic animals and cells, and for
CC producing engineered lung tissue for treatment and research. (II) is also
CC useful for detecting or amplifying nucleic acid molecules that have
CC similar or identical nucleic acid sequences compared to (II). (I) is
CC useful for producing engineered lung tissue. (V) is useful for
CC identifying (I). (II) is also useful for driving in vivo expression of
CC (I). The present sequence represents a human LSP from the present
CC invention.
XX
SQ Sequence 532 AA;

Query Match 100.0%; Score 31; DB 7; Length 532;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5
|||||
Db 186 HKNQY 190

RESULT 11

ADJ49639

ID ADJ49639 standard; protein; 1998 AA.

XX

AC ADJ49639;

XX

DT 06-MAY-2004 (first entry)

XX

DE Oil-associated gene related protein #1139.

XX

KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX

OS Unidentified.

XX

PN US2004025202-A1.

XX

PD 05-FEB-2004.

XX

PF 14-MAR-2003; 2003US-00389566.

XX

PR 15-MAR-2002; 2002US-0365301P.

PR 26-JUN-2002; 2002US-0391786P.

PR 26-JUN-2002; 2002US-0392018P.

XX

PA (LAUR/) LAURIE C C.

PA (RAVA/) RAVANELLO M.

PA (SAVA/) SAVAGE T.

PA (LEDE/) LEDEAUX J R.

PA (ROGE/) ROGERS J A.

XX

PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX

DR WPI; 2004-142683/14.

XX

PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.

XX

PS Example 3; SEQ ID NO 1643; 22pp; English.

XX

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid

CC sequence of an oil-associated gene related protein.

XX

SQ Sequence 1998 AA;

Query Match 100.0%; Score 31; DB 8; Length 1998;

Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQY 5

||||

Db 1348 HKNQY 1352

RESULT 12

AAM82072

ID AAM82072 standard; protein; 50 AA.

XX

AC AAM82072;

XX

DT 13-NOV-2001 (first entry)

XX

DE Human haematological malignancy-related antigen #1770.

XX

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

KW haematological malignancy; antigen; chronic lymphocytic leukaemia;

KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

XX

OS Homo sapiens.

XX

PN WO200164886-A2.

XX

PD 07-SEP-2001.

XX

PF 01-MAR-2001; 2001WO-US007272.

XX

PR 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 28-APR-2000; 2000US-0200779P.

PR 01-MAY-2000; 2000US-0200999P.

PR 04-MAY-2000; 2000US-0202084P.

PR 22-MAY-2000; 2000US-0206201P.

PR 14-JUL-2000; 2000US-0218950P.

PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.

PR 07-AUG-2000; 2000US-0223378P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Gaiger A, Algate PA, Mannion J;

XX

DR WPI; 2001-514842/56.

XX

PT Compositions and methods for the detection of hematological malignancies,

PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and

PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

XX

PS Claim 1; Page 1215; 1252pp; English.

XX

CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma

XX

SQ Sequence 50 AA;

Query Match 90.3%; Score 28; DB 4; Length 50;

Best Local Similarity 80.0%; Pred. No. 86;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKNQY 5

|:|

Db 26 HRNQY 30

Search completed: October 26, 2004, 19:35:46

Job time : 161 secs